PATENT
Attorney Docket No. **FORS-06137**

REMARKS

Claims 1-2, 4-16, 18-23 and 25-28 are at issue in the present application. Claims 16 and 18-20 have been rejected and Claims 1-2, 4-15, 21-23 and 25-28 are allowed. For the Examiner's convenience, a copy of the pending claims is attached to this communication as an appendix. Applicants note that all amendments and canceling of Claims presented herein are made without acquiescing to any of the Examiner's arguments or rejections, and solely for the purpose of expediting the patent application process in a manner consistent with the PTO's Patent Business Goals (PBG),[1] and without waiving the right to prosecute the amended or canceled Claims (or similar Claims) in the future.

The Examiner has rejected Claims 16 and 18-20 under 35 U.S.C. 112, second paragraph as allegedly being indefinite because the "method steps of claims 16 and 18-20 lack antecedent basis in the preamble to claim 16." (Office Action, pg. 2). The Applicants respectfully disagree. However, in order to expedite the prosecution process, the Applicants have amended Claim 16 to link the preamble to the method steps. This amendment renders the indefiniteness rejection moot, and the Applicants request that the rejection be withdrawn.

CONCLUSION

All grounds of rejection of the Office Action of February 26, 2002 having been addressed, it is respectfully submitted that the invention as claimed fully meets all requirements and that the claims should be passed to allowance. Should the Examiner have any questions, or if a telephone conference would aid in the prosecution of the present application, Applicant encourages the Examiner to call the undersigned collect at 608-218-6900.

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[1] 65 Fed. Reg. 54603 (Sept. 8, 2000).

Appendix
Pending Claims

1. A method for identifying the presence of a nucleic acid target in a sample by determination of structure formation with said nucleic acid target, comprising the steps of:

a) providing:

i) a sample suspected of having a folded target having a deoxyribonucleic acid sequence comprising one or more double stranded regions, and one or more single stranded regions, and further comprising two or more non-contiguous portions, and one or more intervening regions; and

ii) one or more bridging oligonucleotide probes complementary to said two or more non-contiguous portions of said folded target; and

b) mixing said folded target and said one or more probes under conditions such that said probe hybridizes to said folded target to form a probe/folded target complex; and

c) detecting said probe/folded target complex, thereby detecting the presence of said folded target in said sample.

2. The folded target of Claim 1, wherein said one or more intervening regions comprises at least five nucleotides.

4. The method of Claim 1, further comprising quantitating the amount of probe/folded target complex formed.

5. The method of Claim 1, wherein said probe in said probe/folded target complex is hybridized to at least one single stranded region of said folded target.

6. The method of Claim 1, wherein said bridging oligonucleotide probe further comprises a moiety that permits the capture of said bridging oligonucleotide probe by a solid support.

7. The method of Claim 6, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid support under conditions such that said bridging oligonucleotide is captured by said solid support.

8. The method of Claim 7, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

9. The method of Claim 1, wherein said folded target is labelled.

10. The method of Claim 1, wherein said folded target comprises a deoxyribonucleic acid sequence having a moiety that permits its capture by a solid support.

11. The method of Claim 10, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid support under conditions such that said folded target is captured by said solid support.

12. The method of Claim 11, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

13. The method of Claim 1, wherein said bridging oligonucleotide probe is labelled.

14. The method of Claim 1, wherein said bridging oligonucleotide probe is attached to a solid support.

15. The method of Claim 1, wherein said folded target nucleic acid is attached to a solid support.

16. A method for comparing the amount of probe/folded target complexes, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first and second portions, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target and a second portion that differs from said second portion of

said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) first and second bridging oligonucleotides said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and said second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

b) contacting said first folded target with said first bridging oligonucleotide under conditions such that said first bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a first mixture;

c) contacting said first folded target with said second bridging oligonucleotide under conditions such that said second bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a second mixture;

d) contacting said second folded target with said first bridging oligonucleotide to form a third mixture;

e) contacting said second folded target with said second bridging oligonucleotide to form fourth mixture; and

f) comparing the amount of probe/folded target complex in said first, second, third, and fouth mixtures.

18. The method of Claim 16, wherein the hybridization of said first bridging oligonucleotide in step d) to said second folded target is reduced relative to the hybridization of said first bridging oligonucleotide in step c) to said first folded target.

19. The method of Claim 16, wherein said first and second targets comprise DNA.

20. The method of Claim 16, wherein said first and second bridging oligonucleotides comprise DNA.

21. A method for analyzing folded nucleic acid targets, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first

and second portions, wherein said first and second portions each comprise one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target, and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) a solid support comprising comprising immobilized first and second bridging oligonucleotides, said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

b) contacting said first and second folded targets with said solid support under conditions such that said first and second bridging oligonucleotides hybridize to said first folded target to form a probe/folded target complex; and

c) analyzing the amount of probe/folded target complex formed on said solid support at said first and second testing zones.

22. The method of Claim 21, wherein said contacting of step b) comprises adding said first folded target to said first testing zone and adding said second folded target to said second testing zone.

23. The method of Claim 21, wherein said first and second bridging oligonucleotides are immobilized in separate portions of said testing zones.

25. The method of Claim 23, wherein said first bridging oligonucleotide in said second testing zone hybridizes to said second folded target with a reduced efficiency compared to the hybridization of said first bridging oligonucleotide in first testing zone to said first folded target.

26. The method of Claim 21, wherein said first and second folded targets comprise DNA.

27. The method of Claim 21, wherein said first and second folded targets comprise RNA.

28. The method of Claim 21, wherein said first and second bridging oligonucleotides comprise DNA.